SEQ ID 2	1	ATG	TTG	CAG	ATG	GCT	GGG	CAG	TGC	TCC	CAA	AAT	GAA	TAT	TTT	GAC	AGT	TTG	TTG	CAT	GCT
SEQ ID 1	1▸	M	L	Q	M	A	G	Q	C	S	Q	N	E	Y	F	D	S	L	L	H	A
	61	TGC	ATA	CCT	TGT	CAA	CTT	CGA	TGT	TCT	TCT	AAT	ACT	CCT	CCT	CTA	ACA	TGT	CAG	CGT	TAT
	21▸	C	I	P	C	Q	L	R	C	S	S	N	T	P	P	L	T	C	Q	R	Y
	121	TGT	AAT	GCA	AGT	GTG	ACC	AAT	TCA	GTG	AAA	GGA	ACG	AAT	GCG	ATT	CTC	TGG	ACC	TGT	TTG
	41▸	C	N	A	S	V	T	N	S	V	K	G	T	N	A	I	L	W	T	C	L
	181	GGA	CTG	AGC	TTA	ATA	ATT	TCT	TTG	GCA	GTT	TTC	GTG	CTA	ATG	TTT	TTG	CTA	AGG	AAG	ATA
	61▸	G	L	S	L	I	I	S	L	A	V	F	V	L	M	F	L	L	R	K	I
	241	AGC	TCT	GAA	CCA	TTA	AAG	GAC	GAG	TTT	AAA	AAC	ACA	GGA	TCA	GGT	CTC	CTG	GGC	ATG	GCT
	81▸	S	S	E	P	L	K	D	E	F	K	N	T	G	S	G	L	L	G	M	A
	301	AAC	ATT	GAC	CTG	GAA	AAG	AGC	AGG	ACT	GGT	GAT	GAA	ATT	ATT	CTT	CCG	AGA	GGC	CTC	GAG
	101▸	N	I	D	L	E	K	S	R	T	G	D	E	I	I	L	P	R	G	L	E
	361	TAC	ACG	GTG	GAA	GAA	TGC	ACC	TGT	GAA	GAC	TGC	ATC	AAG	AGC	AAA	CCG	AAG	GTC	GAC	TCT
	121▸	Y	T	V	E	E	C	T	C	E	D	C	I	K	S	K	P	K	V	D	S
	421	GAC	CAT	TGC	TTT	CCA	CTC	CCA	GCT	ATG	GAG	GAA	GGC	GCA	ACC	ATT	CTT	GTC	ACC	ACG	AAA
	141▸	D	H	C	F	P	L	P	A	M	E	E	G	A	T	I	L	V	T	T	K
	481	ACG	AAT	GAC	TAT	TGC	AAG	AGC	CTG	CCA	GCT	GCT	TTG	AGT	GCT	ACG	GAG	ATA	GAG	AAA	TCA
	161▸	T	N	D	Y	C	K	S	L	P	A	A	L	S	A	T	E	I	E	K	S
	541	ATT	TCT	GCT	AGG	TAA															
	181▸	I	S	A	R	•															

FIG. 1

FIG. 2A

FIG. 2B

FIG. 2

```
              1  ATG GAG ACA GAC ACA CTC CTG TTA TGG GTG CTG CTG CTC TGG GTT CCA GGT TCC ACT GGT
             1▸
SEQ ID 4     1▸  M   E   T   D   T   L   L   L   W   V   L   L   L   W   V   P   G   S   T   G
SEQ ID 3    61  GAC GTC ACG ATG TTG CAG ATG GCT GGG CAG TGC TCC CAA AAT GAA TAT TTT GAC AGT TTG
                          1▸ M   L   Q   M   A   G   Q   C   S   Q   N   E   Y   F   D   S   L
            21▸  D   V   T   M   L   Q   M   A   G   Q   C   S   Q   N   E   Y   F   D   S   L
           121  TTG CAT GCT TGC ATA CCT TGT CAA CTT CGA TGT TCT TCT AAT ACT CCT CCT CTA ACA TGT
            18▸  L   H   A   C   I   P   C   Q   L   R   C   S   S   N   T   P   P   L   T   C
            41▸  L   H   A   C   I   P   C   Q   L   R   C   S   S   N   T   P   P   L   T   C
           181  CAG CGT TAT TGT AAT GCA AGT GTG ACC AAT TCA GTG AAA GGA GTC GAC AAA ACT CAC ACA
            38▸  Q   R   Y   C   N   A   S   V   T   N   S   V   K   G
            61▸  Q   R   Y   C   N   A   S   V   T   N   S   V   K   G   V   D   K   T   H   T
           241  TGC CCA CCG TGC CCA GCA CCT GAA CTC CTG GGG GGA CCG TCA GTC TTC CTC TTC CCC CCA

            81▸  C   P   P   C   P   A   P   E   L   L   G   G   P   S   V   F   L   F   P   P
           301  AAA CCC AAG GAC ACC CTC ATG ATC TCC CGG ACC CCT GAG GTC ACA TGC GTG GTG GTG GAC

           101▸  K   P   K   D   T   L   M   I   S   R   T   P   E   V   T   C   V   V   V   D
           361  GTG AGC CAC GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC GTG GAG GTG CAT

           121▸  V   S   H   E   D   P   E   V   K   F   N   W   Y   V   D   G   V   E   V   H
           421  AAT GCC AAG ACA AAG CCG CGG GAG GAG CAG TAC AAC AGC ACG TAC CGT GTG GTC AGC GTC

           141▸  N   A   K   T   K   P   R   E   E   Q   Y   N   S   T   Y   R   V   V   S   V
           481  CTC ACC GTC CTG CAC CAG GAC TGG CTG AAT GGC AAG GAG TAC AAG TGC AAG GTC TCC AAC
```

FIG. 2A

```
161▶ L  T  V  L  H  Q  D  W  L  N  G  K  E  Y  K  C  K  V  S  N
541  AAA GCC CTC CCA GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA GGG CAG CCC CGA GAA

181▶ K  A  L  P  A  P  I  E  K  T  I  S  K  A  K  G  Q  P  R  E
601  CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG GAT GAG CTG ACC AAG AAC CAG GTC AGC CTG

201▶ P  Q  V  Y  T  L  P  P  S  R  D  E  L  T  K  N  Q  V  S  L
661  ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC GAC ATC GCC GTG GAG TGG GAG AGC AAT GGG

221▶ T  C  L  V  K  G  F  Y  P  S  D  I  A  V  E  W  E  S  N  G
721  CAG CCG GAG AAC AAC TAC AAG ACC ACG CCT CCC GTG TTG GAC TCC GAC GGC TCC TTC TTC

241▶ Q  P  E  N  N  Y  K  T  T  P  P  V  L  D  S  D  G  S  F  F
781  CTC TAC AGC AAG CTC ACC GTG GAC AAG AGC AGG TGG CAG CAG GGG AAC GTC TTC TCA TGC

261▶ L  Y  S  K  L  T  V  D  K  S  R  W  Q  Q  G  N  V  F  S  C
841  TCC GTG ATG CAT GAG GCT CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC TCC CTG TCT CCC

281▶ S  V  M  H  E  A  L  H  N  H  Y  T  Q  K  S  L  S  L  S  P
901  GGG AAA TGA

301▶ G  K  •
```

FIG. 2B

```
                                                      BsaAI       BbsI
  1 AAGACTCAAA CTTAGAAACT TGAATTAGAT GTGGTATTCA AATCCTTACG TGCCGCGAAG
 61 ACACAGACAG CCCCCGTAAG AACCCACGAA GCAGGCGAAG TTCATTGTTC TCAACATTCT
                                 EcoRI
121 AGCTGCTCTT GCTGCATTTG CTCTGGAATT CTTGTAGAGA TATTACTTGT CCTTCCAGGC
               SfcI                         BclI
181 TGTTCTTTCT GTAGCTCCCT TGTTTTCTTT TTGTGATCAT GTTGCAGATG GCTGGGCAGT
                                            1▶ M   L  Q  M   A  G  Q
                      SspI               SphI              HincII
241 GCTCCCAAAA TGAATATTTT GACAGTTTGT TGCATGCTTG CATACCTTGT CAACTTCGAT
  8▶C  S  Q  N   E  Y  F   D  S  L   L  H  A  C   I  P  C   Q  L  R
                                 Pci I
                                 AflIII
301 GTTCTTCTAA TACTCCTCCT CTAACATGTC AGCGTTATTG TAATGCAAGT GTGACCAATT
 28▶C  S  S  N   T  P  P   L  T  C   Q  R  Y  C   N  A  S   V  T  N
                                              BsmFI
361 CAGTGAAAGG AACGAATGCG ATTCTCTGGA CCTGTTTGGG ACTGAGCTTA ATAATTTCTT
 48▶S  V  K  G   T  N  A   I  L  W   T  C  L  G   L  S  L   I  I  S
421 TGGCAGTTTT CGTGCTAATG TTTTTGCTAA GGAAGATAAG CTCTGAACCA TTAAAGGACG
 68▶L  A  V  F   V  L  M   F  L  L   R  K  I  S   S  E  P   L  K  D
      DraI          AlwI    BsaI
481 AGTTTAAAAA CACAGGATCA GGTCTCCTGG GCATGGCTAA CATTGACCTG GAAAAGAGCA
 88▶E  F  K  N   T  G  S   G  L  L   G  M  A  N   I  D  L   E  K  S
                 XmnI                StuI  XhoI
541 GGACTGGTGA TGAAATTATT CTTCCGAGAG GCCTCGAGTA CACGGTGGAA GAATGCACCT
108▶R  T  G  D   E  I  I   L  P  R   G  L  E  Y   T  V  E   E  C  T
                                      SalI
                                      HincII
      BbsI                            AccI
601 GTGAAGACTG CATCAAGAGC AAACCGAAGG TCGACTCTGA CCATTGCTTT CCACTCCCAG
128▶C  E  D  C   I  K  S   K  P  K   V  D  S  D   H  C  F   P  L  P
661 CTATGGAGGA AGGCGCAACC ATTCTTGTCA CCACGAAAAC GAATGACTAT TGCAAGAGCC
148▶A  M  E  E   G  A  T   I  L  V   T  T  K  T   N  D  Y   C  K  S
       PvuII
721 TGCCAGCTGC TTTGAGTGCT ACGGAGATAG AGAAATCAAT TTCTGCTAGG TAATTAACCA
168▶L  P  A  A   L  S  A   T  E  I   E  K  S  I   S  A  R
         XhoI               DraI                                BglII
781 TTTCGACTCG AGCAGTGCCA CTTTAAAAAT CTTTTGTCAG AATAGATGAT GTGTCAGATC
841 TCTTTAGGAT GACTGTATTT TTCAGTTGCC GATACAGCTT TTTGTCCTCT AACTGTGGAA
                                                                   StyI
901 ACTCTTTATG TTAGATATAT TTCTCTAGGT TACTGTTGGG AGCTTAATGG TAGAAACTTC
961 CTTGGTTTCA TGATTAAAGT CTTTTTTTTT CCTGA
```

FIG. 3

SRUCTURE COMPARISON BETWEEN TNF-R55 AND BAFF-R

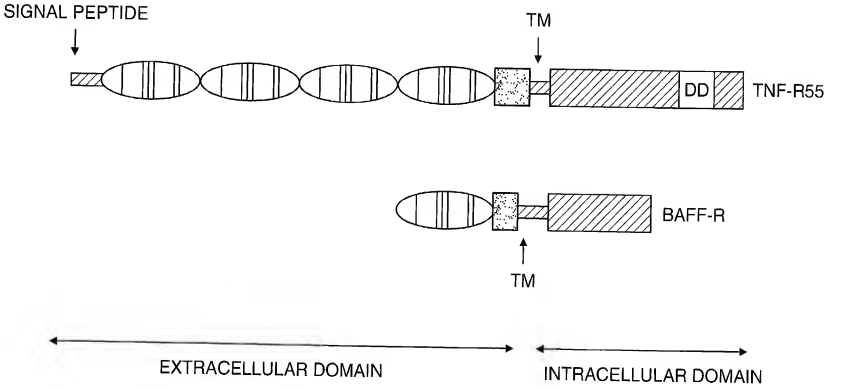


FIG. 4

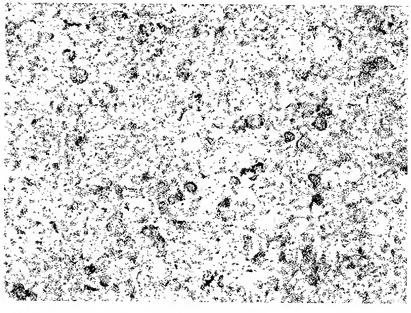


FIG. 5A

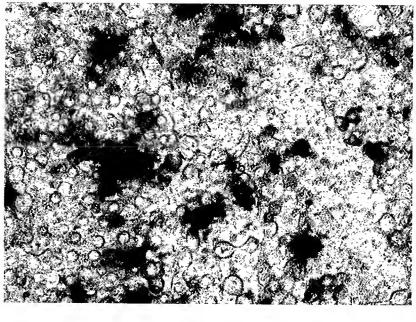


FIG. 5B

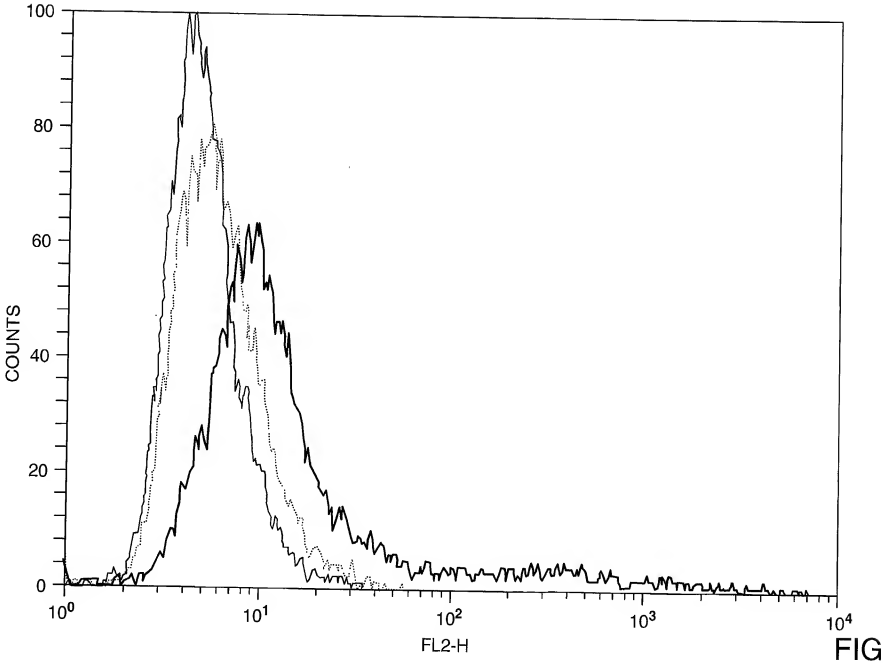
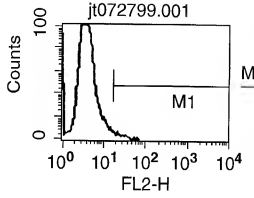
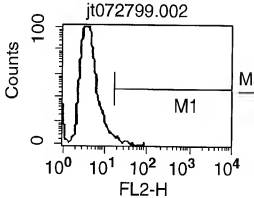


FIG. 6A



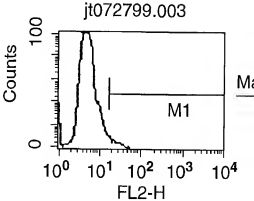
Marker	Left	Right	Events	% Gated	% Total	Mean	Geo Mean	CV	Median
All	1.	9910	10000	100.00	100.00	4.26	3.80	61.34	3.65
M1	17.	9910	65	0.65	0.65	23.23	22.44	30.37	20.35

FIG. 6B-1



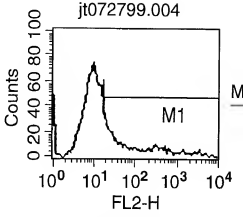
Marker	Left	Right	Events	% Gated	% Total	Mean	Geo Mean	CV	Median
All	1.	9910	10000	100.00	100.00	4.61	4.11	61.98	3.89
M1	17.	9910	79	0.79	0.79	22.88	21.98	34.94	19.63

FIG. 6B-2



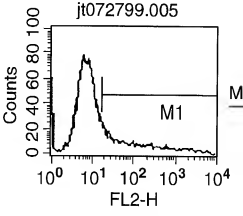
Marker	Left	Right	Events	% Gated	% Total	Mean	Geo Mean	CV	Median
All	1.	9910	10000	100.00	100.00	5.51	4.93	58.41	4.66
M1	17.	9910	130	1.30	1.30	23.55	22.98	23.39	22.57

FIG. 6B-3



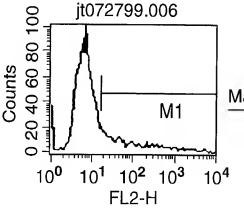
Marker	Left	Right	Events	% Gated	% Total	Mean	Geo Mean	CV	Median
All	1.	9910	10000	100.00	100.00	108.24	15.40	459.27	10.27
M1	17.	9910	2785	27.85	27.85	366.10	85.21	243.61	45.32

FIG. 6B-4



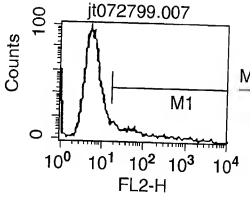
Marker	Left	Right	Events	% Gated	% Total	Mean	Geo Mean	CV	Median
All	1.	9910	10000	100.00	100.00	72.53	11.42	516.47	7.84
M1	17.	9910	2054	20.54	20.54	324.52	88.86	239.37	61.80

FIG. 6B-5



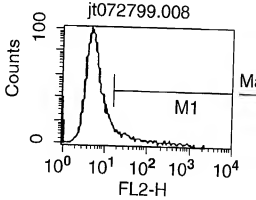
Marker	Left	Right	Events	% Gated	% Total	Mean	Geo Mean	CV	Median
All	1.	9910	10000	100.00	100.00	51.15	9.41	566.98	6.67
M1	17.	9910	1673	16.73	16.73	272.40	81.97	244.63	54.25

FIG. 6B-6



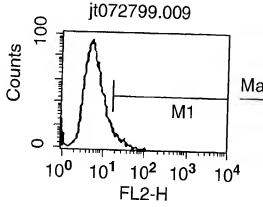
Marker	Left	Right	Events	% Gated	% Total	Mean	Geo Mean	CV	Median
All	1.	9910	10000	100.00	100.00	26.59	7.74	576.94	5.94
M1	17.	9910	1313	13.13	13.13	161.35	60.77	246.67	42.94

FIG. 6B-7



Marker	Left	Right	Events	% Gated	% Total	Mean	Geo Mean	CV	Median
All	1.	9910	10000	100.00	100.00	12.39	6.54	405.32	5.47
M1	17.	9910	876	8.76	8.76	78.94	43.41	195.84	33.68

FIG. 6B-8



Marker	Left	Right	Events	% Gated	% Total	Mean	Geo Mean	CV	Median
All	1.	9910	10000	100.00	100.00	6.99	6.60	69.06	5.67
M1	17.	9910	393	3.93	3.93	24.33	23.31	33.78	21.48

FIG. 6B-9


1 2 3 4 5 6 7
57
43
29
23
18

FIG. 7

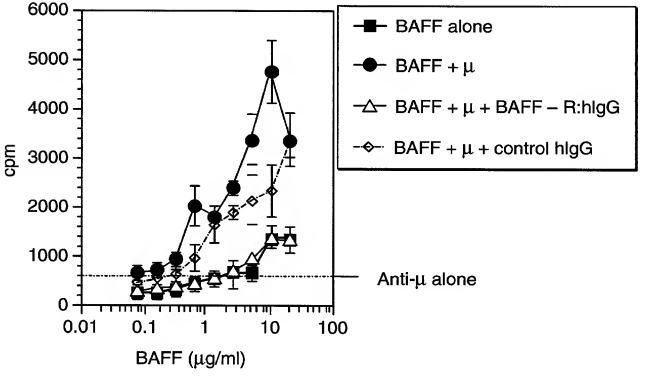

6000
5000
4000
3000
2000
1000
0
cpm
0.01
0.1
1
10
100
BAFF (μg/ml)
BAFF alone
BAFF + μ
BAFF + μ + BAFF – R:hIgG
BAFF + μ + control hIgG
Anti-μ alone

FIG. 8

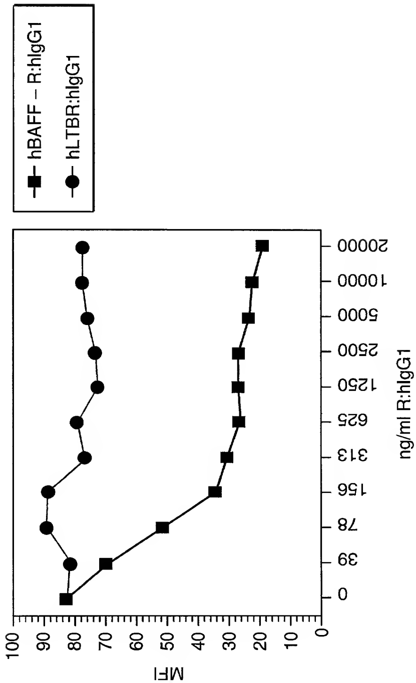

hBAFF – R:hIgG1
hLTBR:hIgG1
MFI
100
90
80
70
60
50
40
30
20
10
0
0
39
78
156
313
625
1250
2500
5000
10000
20000
ng/ml R:hIgG1

FIG. 9

FIG. 10A

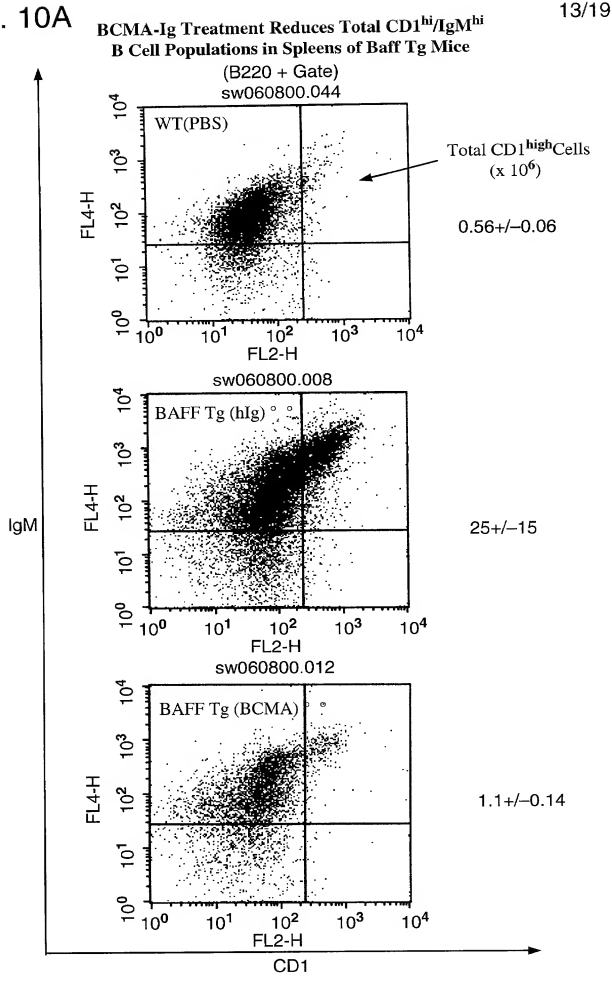


FIG. 10B

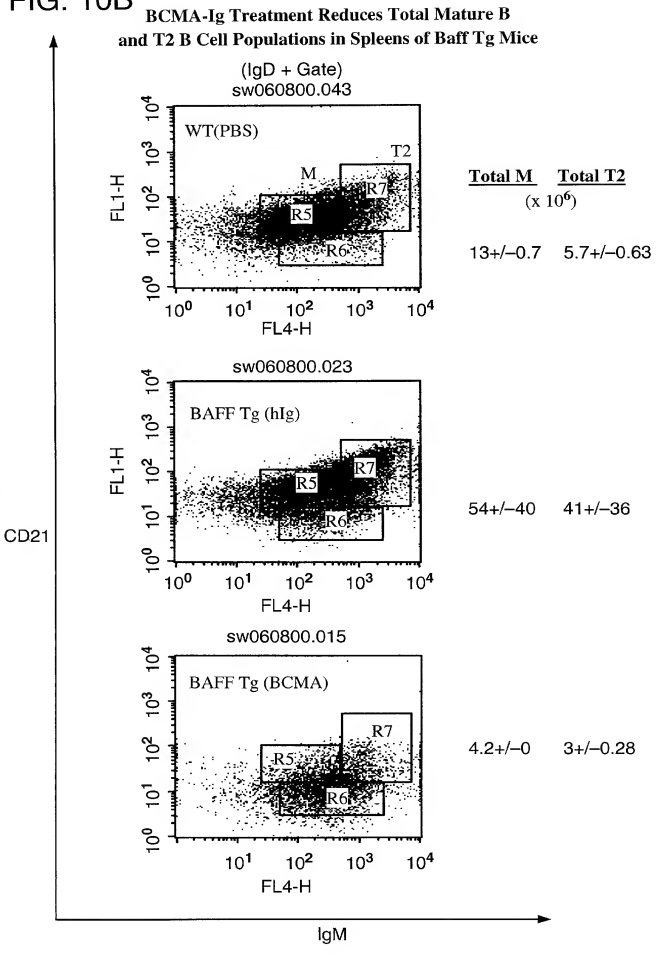
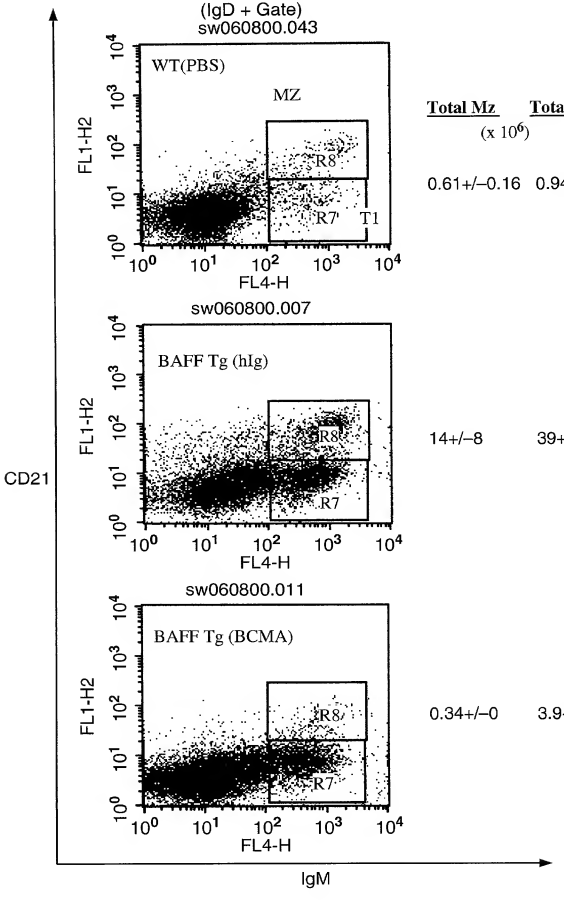


FIG. 10C

BCMA-Ig Treatment Reduces Total Marginal Zone and T1 B Cell Populations in Spleens of Baff Tg Mice



	Total Mz (x 10^6)	Total T1
WT(PBS)	0.61+/–0.16	0.94+/–0.08
BAFF Tg (hIg)	14+/–8	39+/–20
BAFF Tg (BCMA)	0.34+/–0	3.9+/–1.8

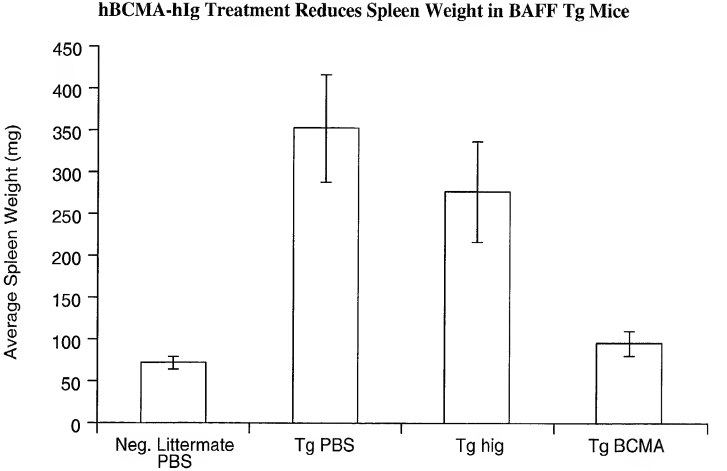


FIG. 11

BCMA-Ig Treatment Reduces Proteinurea in BAFF Tg Mice to Levels Comparable to Wildtype Mice

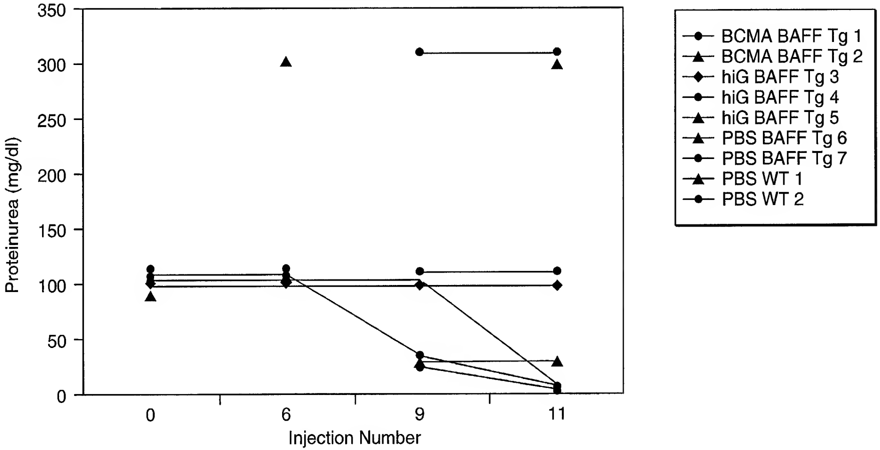


FIG. 12

Average Mean Arterial Pressure in BAFF transgenic (BAFF +) and wild-type controls (BAFF –)

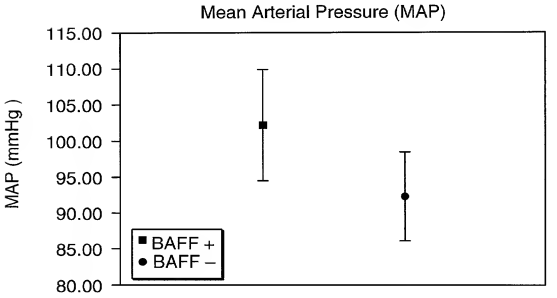


FIG. 13

Individual Mean Arterial Pressure in BAFF transgenic (BAFF +) and wild-type controls (BAFF –)

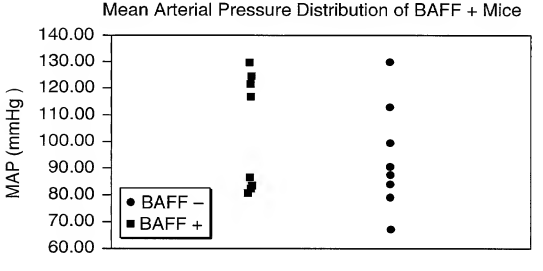


FIG. 14

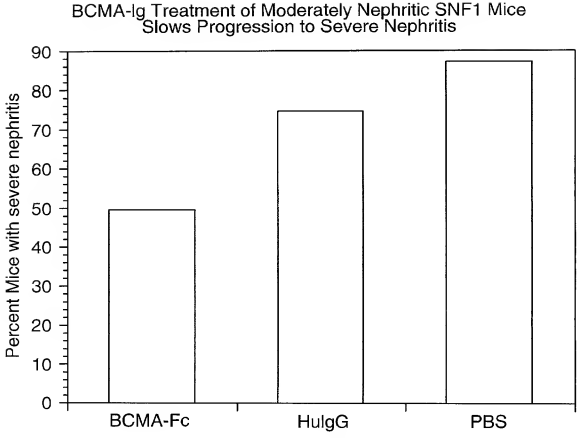

BCMA-Ig Treatment of Moderately Nephritic SNF1 Mice
Slows Progression to Severe Nephritis
Percent Mice with severe nephritis
0
10
20
30
40
50
60
70
80
90
BCMA-Fc
HulgG
PBS

FIG. 15

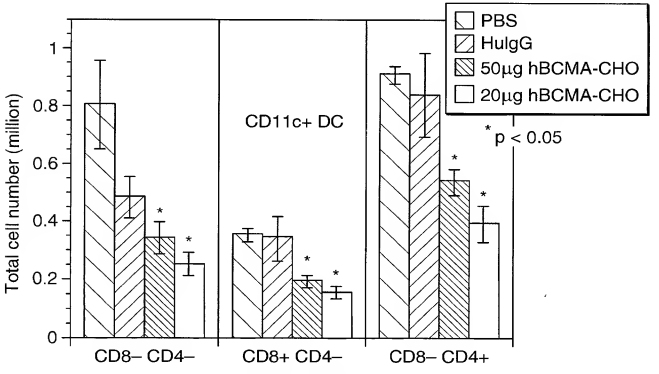

PBS
HulgG
50μg hBCMA-CHO
20μg hBCMA-CHO
Total cell number (million)
0
0.2
0.4
0.6
0.8
1
CD11c+ DC
* p < 0.05
CD8– CD4–
CD8+ CD4–
CD8– CD4+

FIG. 16